A novel relaxase homologue is involved in chromosomal DNA processing for type IV secretion in Neisseria gonorrhoeae

Salgado-Pabon, Wilmara; Jain, Samta; Turner, Nicholas; van der Does, Chris; Dillard, Joseph P.

Published in:
Molecular Microbiology

DOI:
10.1111/j.1365-2958.2007.05966.x

Publication date:
2007

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P.rettgeri |AAM08003.1|                    --------------------------------------------------
V.cholerae MO10 |EAZ47260.1|               --------------------------------------------------
V.cholerae |ABA87024.1|                    --------------------------------------------------
Shewanella W3-18-1 |YP_962502.1|           --------------------------------------------------
Y.p.orientalis IP275 |ZP_01175343.1|       --------------------------------------------------
X.c.vesicatoria 85-10 |YP_364087.1|       --------------------------------------------------
Acidovorax JS42 |ZP_01384863.1|           --------------------------------------------------
X.fastidiosa 9a5c |NP_299042.1|           --------------------------------------------------
Acidovorax JS42 |ZP_01382702.1|           --------------------------------------------------
P.aeruginosa PACS2 |ZP_01366009.1|        --------------------------------------------------
R.metallidurans CH34 |YP_584510.1|        -MTLESHPVPRYTETVKGQRAEMARERGARGKALPRKGQKASRSARHQDT 49
P.aeruginosa 2192 |ZP_00974810.1|         --------------------------------------------------
P.aeruginosa str.C |AAN62129.1|           --------------------------------------------------
B.xenovorans LB400 |YP_559832.1|          --------------------------------------------------
X.c.campestris ATCC33913 |NP_638468.1|   --------------------------------------------------
N.eutropha C91 |ABI58357.1|               --------------------------------------------------
X.c.campestris 8004 |YP_243101.1|        --------------------------------------------------
P.aeruginosa SG17M |AAN62266.1|           --------------------------------------------------
R.gelatinosus PM1 |ZP_00242313.1|        --------------------------------------------------
Acidovorax JS42 |ZP_01384808.1|          --------------------------------------------------
Azoarcus EbN1 |YP_158431.1|              --------------------------------------------------
Azoarcus EbN1 |YP_158356.1|              --------------------------------------------------
A.a.citrulli AAC00-1 |ZP_01405034.1|     --------------------------------------------------
X.a.citri 306 |NP_642513.1|              --------------------------------------------------
P.aeruginosa PA14 |AAP84130.1|           ------------------------------------------------MF 2
P.aeruginosa 6077 |ABD94612.1|           ----------------------------------------------MELPMF 6
P.aeruginosa C pKLC102 |AAP22591.1|     ------------------------------------------------MF 2
P.aeruginosa C |AAP94681.1|              --------------------------------------------------
P.aeruginosa 2192 |ZP_00971291.1|        --------------------------------------------------
A.vinelandii AvOP |ZP_00419624.1|        -------------------------------------------------M 1
P.fluorescens Pf-5 |YP_261833.1|         -------------------------------------------------M 1
P.s.phaseolicola |CAI36140.1|           --------------------------------------------------
P.syringae BR2R |AAL99262.1|            ----------------------------------------------MGA 3
P.s.tomato DC3000 |NP_790676.1|         ----------------------------------------------MGT 3
P.s.syringae B728a |YP_233835.1|        --------------------------------------------------
P.putida F1 |ZP_00898124.1|             --------------------------------MEGGARVRGLSEKAKGPFE 19
P.fluorescens PfO-1 |YP_348763.1|       --------------------------------------------------
H.influenzae R2866 |ZP_00157643.1|      --------------------------------------------------
H.influenzae pICEhin1056|CAF29070.1|   --------------------------------------------------
H.influenzae 86-028NP |YP_247808.1|     -------------------------------------------------M 1
H.ducreyi 35000HP |NP_873395.1|         --------------------------------------------------
H.somnus 129PT |YP_718205.1|           --------------------------------------------------
M.aquaeolei VT8 |ZP_00817690.1|         -------------------------------------------------M 1
A.a.citrulli AAC00-1 |ZP_01407598.1|   --------MDARGRQSRSRPALFHPTAGAGSRHAVNSVAARLLRLLPWSR 42
Azoarcus EbN1 |YP_157225.1|            ----------------------MAMLAAG----FLLVAAVLAVWLIWAS 23
E.coli pAPEC-O1-R |ABF67837.1|         ------------------MMMNFRALYLCIKRILGIFSSQENDATSVMIE 32
S.marcescens R478 |NP_941280.1|        ------------------MMMNFRALYLCIKRILGIFSSQENDATSVMIE 32
S.typhi R27 |NP_058333.1|              --------------------MNFRALFLSMQRVFGIFSRRENDVSELMMK 30
S.e.e.typhi CT18 pHCM1 |NP_569454.1|   --------------------MNFRALFLSMQRVFGIFSRRENDVSELMMK 30
N.gonorrhoeae MS11 |AAW83058.1|        ------------------------------------------MKTSLLTIASS 11
P.resinovorans pCAR1 |NP_758664.1|    MRRSKSRHSFSEPSGSNPSARHLPGFFSTIKLPENETQGGIPHASFSAHN 50
P.vulgaris UR-75 pRts1 |NP_640161.1|   --------------------------------------------------
Consensus                              ..................................................
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P.rettgeri |AAM08003.1|                    ----MFKNLFFQTKALPELS---------SQLDADIPRYPPFLKGLPAAS 37
V.cholerae MO10 |EAZ47260.1|              ----MFKNLFFQAKALPDLS---------SQLDAEIPRYPPFLKGLPAAS 37
V.cholerae |ABA87024.1|                   ----MFKNLFFQAKALPELS---------SQLDAEIPRYPPFLKGLPAAS 37
Shewanella W3-18-1 |YP_962502.1|          ----MFKKLFFQAKAIPELS---------SQLDADIPRYPPFLKGLPAAS 37
Y.p.orientalis IP275 |ZP_01175343.1|      -MLKALNKLFGGRSGVIETAPSARVLPLKDVEDEEIPRYPPFAKGLPVAP 49
X.c.vesicatoria 85-10 |YP_364087.1|       ----MLS---LFQRKRPPVAAAP-------SPPPAIDLPKGLMRPESAAS 36
Acidovorax JS42 |ZP_01384863.1|           ----MLS---LFQRKRPPVAAAP-------SPPPAIDLPKGLMRPESAAS 36
X.fastidiosa 9a5c |NP_299042.1|           ----MLS---LFQRKRPPVAATP-------SPAPATDLPKGLMRPESTAS 36
Acidovorax JS42 |ZP_01382702.1|           ----MLS---LFQRKRPAVAAAP-------TPPSVTDLPKGLMRPESAAS 36
P.aeruginosa PACS2 |ZP_01366009.1|        ----MLF---LFQRKRPPVAAAP-------SPAPALDLPKGLLRPESAAS 36
R.metallidurans CH34 |YP_584510.1|        ---HMLS---LFQRKRPAVATAP-------TPPPASDLPKGLMRPESAAS 86
P.aeruginosa 2192 |ZP_00974810.1|         ----------------------------------------MRPESAAS 8
P.aeruginosa str.C |AAN62129.1|           ----MLS---LFQRKRPAVATAP-------TPPPASDLPKGLMRPESAAS 36
B.xenovorans LB400 |YP_559832.1|          ----MLS---LFQRKRPVVASAP-------SPAPSNDLPKGRLRPESAAS 36
X.c.campestrisATCC33913|NP_638468.1|     ----MLR---LFQRK-SAVLPPV-------AAVTETALSKGLLQPKPAAE 35
N.eutropha C91 |ABI58357.1|               ----MLS---LFQRKRLLPTTDM-------APMPSTAPPKGPMRPESAAS 36
X.c.campestris 8004 |YP_243101.1|        ----MLS---LFQRKRASVAAAA-------SPGPTTDLPKGLTRPETAAS 36
P.aeruginosa SG17M |AAN62266.1|          ----MLS---LLQRKRVSPTAGA-------PATPASDSPKRLTQPESATA 36
R.gelatinosus PM1 |ZP_00242313.1|        ----------------------------------------MRPESAAS 8
Acidovorax JS42 |ZP_01384808.1|          ----MLS---LFQRKRVPPTAGT-------PPTSAIETPKGSMRPESAAS 36
Azoarcus EbN1 |YP_158431.1|             ----MIS---LFQRKRVPPATGA-------PPT-LTEPPKGLMRPASAAS 35
Azoarcus EbN1 |YP_158356.1|             ----MLS---LFQRKRVTPTVGA-------PITPPPEAPKGLMGPESAAS 36
A.a.citrulli AAC00-1 |ZP_01405034.1|     ----MFR---LFRRAAGAASTTERTPANAPPVAATTPSLPGWTARQSASE 43
X.a.citri 306 |NP_642513.1|              ----MFRPFQLFQRAGRQASTIATTCS--PETVPDRGSAPGWRTPLSASE 44
P.aeruginosa PA14 |AAP84130.1|           QLLS------WISRKPSPTPTTKA-------------APGGFILPLSSME 33
P.aeruginosa 6077 |ABD94612.1|           QLLS------WISRKPSPTPPTKA-------------APGGFIPPLSSME 37
P.aeruginosa C pKLC102 |AAP22591.1|     QLLS------WISRKPSPTPPTKA-------------APGVFLLPLSSTE 33
P.aeruginosa C |AAP94681.1|              ------------------------------------------------ME 2
P.aeruginosa 2192 |ZP_00971291.1|        ------------------------------------------------ME 2
A.vinelandii AvOP |ZP_00419624.1|        SLLT------WLGRKSAE-PTSEA-------------PSQGFHSPARAAV 31
P.fluorescens Pf-5 |YP_261833.1|         QILS------WLSRKPAR-PPSEA-------------TAQGFHLPVNAAA 31
P.s.phaseolicola |CAI36140.1|           ------------------------------------------------
P.syringae BR2R |AAL99262.1|            YMLS------FFTRRKAS-PISSN-------------NAAGFFKPESPDA 33
P.s.tomato DC3000 |NP_790676.1|         SMLS------FFQRRKTS-PTTPS-------------NAAGFTKPESADA 33
P.s.syringae B728a |YP_233835.1|        -MLS------FFTRRKAS-PISSN-------------AAAGFFKPESPDA 29
P.putida F1 |ZP_00898124.1|             RKTGTAMKRWWFKPQKGLPEESTP-------------AAVGFHQPLSAES 56
P.fluorescens PfO-1 |YP_348763.1|       -----MLSLFRHKRQKPPPPPTVN-------------VAEGYLSIESAHT 32
H.influenzae R2866 |ZP_00157643.1|      ------------------------------------MDDEGWITPFTASE 14
H.influenzae pICEhin1056|CAF29070.1|   ----MLSSIFHKIRGKKQDSLNITSSLKNLNSSTFKVDDEGWITPFTASE 46
H.influenzae 86-028NP |YP_247808.1|     GYFFMFSSIFYRLKGKKQDSFTIP-VLDSHNHSMSKIDSEGWITPFSASE 50
H.ducreyi 35000HP |NP_873395.1|         -----MISIFHKILNHKNDSKSPTTPIQSQ---QSQTDSDGWLTPLSAKA 42
H.somnus 129PT |YP_718205.1|           ----MFKSLIQFFKSKSNTS---NIKKENAVQRQERQDIEGWITPYSGQE 43
M.aquaeolei VT8 |ZP_00817690.1|         IRPFLVQVSMGFDQNHSAEDSMFKRLMRKELTSSPEPKTPEYAVALSGKD 51
A.a.citrulli AAC00-1 |ZP_01407598.1|    AVAATSPNAGAGAAVTSSGQPPAGDGSAAPTFPRVAGSQPGWLRVLEAEQ 92
Azoarcus EbN1 |YP_157225.1|            YHDRSGRRASCPAAPDAAGSPTATAGDAR----ALAASRPGWLQVLDAST 69
E.coli pAPEC-O1-R |ABF67837.1|          DISSLSPFAQILGDQKYTVPDHPNPEVLKFIEYPTRPTGIQTFNEQSILS 82
S.marcescens R478 |NP_941280.1|         DISSLSPFAQILGDQKYTVPDHPNPEVLKFIEYPTRPTGIQTFNEQSILS 82
S.typhi R27 |NP_058333.1|              DAANFSPFAQIIGEQKYTVPDHPNPEVLKFIEYPTRPAGIQTFNEQSILS 80
S.e.e.typhi CT18 pHCM1 |NP_569454.1|   DAANFSPFAQIIGEQKYTVPDHPNPEVLKFIEYPTRPAGIQTFNEQSILS 80
N.gonorrhoeae MS11 |AAW83058.1|         LMLVSGSMLYLINTRKSTDSVSHN----DEVAHINQNIVNDRFRILNAHE 57
P.resinovorans pCAR1 |NP_758664.1|     MAEKRMPPFSFLKRLWPRSERALTDSFAHPAEQMITPEIKRYLENHNWRN 100
P.vulgaris UR-75 pRts1 |NP_640161.1|   ---MFNRLKTLFSGKRTPKPTVNQIIMPAEVVEALTGSGDILRYPPAELG 47
Consensus                              ................................................
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P.rettgeri |AAM08003.1|                    PEDLQS----------------TQDELIAKLRQ-VLGFNQRDFQRLIQPC 70
V.cholerae MO10 |EAZ47260.1|              PEDLQS----------------TQDELIAKLRQ-VLGFNLRDFQRLIQPC 70
V.cholerae |ABA87024.1|                   PEDLQS----------------TQDELIAKLRQ-VLGFNQREFQRLIQPC 70
Shewanella W3-18-1 |YP_962502.1|          PEELQS----------------TQDELIAKLRQ-VLGFNQRDFQKLIQPC 70
Y.p.orientalis IP275 |ZP_01175343.1|      LDKILA----------------TQAELIEKVRN-SLGFTVDDFNRLVLPV 82
X.c.vesicatoria 85-10 |YP_364087.1|       LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYRAP 68
Acidovorax JS42 |ZP_01384863.1|           LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYRAP 68
X.fastidiosa 9a5c |NP_299042.1|          LLATP-----------------RRQKLMEHIWQ-HTSLSRRQFATLYRAP 68
Acidovorax JS42 |ZP_01382702.1|           LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFATLYRAP 68
P.aeruginosa PACS2 |ZP_01366009.1|        LLATP-----------------RRQKLLEYIWQ-RTSLSRKQFVTLYRTP 68
R.metallidurans CH34 |YP_584510.1|       LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFAVLYRAP 118
P.aeruginosa 2192 |ZP_00974810.1|         LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFAVLYRAP 40
P.aeruginosa str.C |AAN62129.1|           LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFAVLYRAP 68
B.xenovorans LB400 |YP_559832.1|         LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFATLYRAP 68
X.c.campestrisATCC33913|NP_638468.1|    LLATP-----------------RRQKLLEHIWQ-RTSLSRKQFHTLYRVP 67
N.eutropha C91 |ABI58357.1|              LLATP-----------------RRQRLLEHIWQ-RTSLSRKQFASLYRAP 68
X.c.campestris 8004 |YP_243101.1|        LLATP-----------------RRQKLLEHIWQ-RTSLSRQQFDTLYRTP 68
P.aeruginosa SG17M |AAN62266.1|          LLSTP-----------------RRQRLLEHIWQ-RTSLSRQQFTALYLAP 68
R.gelatinosus PM1 |ZP_00242313.1|        LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYLAP 40
Acidovorax JS42 |ZP_01384808.1|          LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYLAP 68
Azoarcus EbN1 |YP_158431.1|             LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYLAP 67
Azoarcus EbN1 |YP_158356.1|             LLATP-----------------RRQKLLEHIWQ-RTSLSRRQFATLYLAP 68
A.a.citrulli AAC00-1 |ZP_01405034.1|    LLAPA-----------------RRQRLLEHIWQ-RTSLSRAQFDQLYLGP 75
X.a.citri 306 |NP_642513.1|             LLAPV-----------------RRQQLIEHIWQ-RTSLSRAQFDALYLAP 76
P.aeruginosa PA14 |AAP84130.1|          LLGTP-----------------RRRQLLENIWQ-RASLSKQQFEEIYRRP 65
P.aeruginosa 6077 |ABD94612.1|          LLGTP-----------------RRRQLLENIWQ-RASLSKQQFEEIYRRP 69
P.aeruginosa C pKLC102 |AAP22591.1|     LLDTP-----------------RRRQLLENIWQ-RASLSKQQFEEIYRRP 65
P.aeruginosa C |AAP94681.1|             LLGTP-----------------RRRQLLENIWQ-RASLSKQQFEEIYRRP 34
P.aeruginosa 2192 |ZP_00971291.1|       LLGTP-----------------RRRQLLENIWQ-RASLSKQQFEEIYRRP 34
A.vinelandii AvOP |ZP_00419624.1|       LFDTP-----------------RRQHLLENIGR-RASLSRQQFDALYRQP 63
P.fluorescens Pf-5 |YP_261833.1|        LLNTP-----------------RRQELLENIWR-RASLSHQQFNTLYRQP 63
P.s.phaseolicola |CAI36140.1|           ---------------------------------------------MQA 3
P.syringae BR2R |AAL99262.1|            LLSSS-----------------RRRQLIENIWQ-RTSLPREQFETLYMQA 65
P.s.tomato DC3000 |NP_790676.1|         LLSTP-----------------RRRQLIENIWQ-RTSLPRTQFDTLYVQA 65
P.s.syringae B728a |YP_233835.1|        LLSTS-----------------RRRQLIENIWQ-RTSLPREQFEALYMQA 61
P.putida F1 |ZP_00898124.1|             LLAAS-----------------HRKKLLARIWQ-YTALSPPQFEQLYLEP 88
P.fluorescens Pf0-1 |YP_348763.1|       LLAVE-----------------HRRQLLDRIWQ-CTALSHVQFTQFYLNP 64
H.influenzae R2866 |ZP_00157643.1|      LLNSE-----------------LRQKYLNLLWQ-QVSMTQDMFNELYKKP 46
H.influenzae pICEhin1056|CAF29070.1|   LLNSE-----------------LRQKYLNLLWQ-QVSMTQDMFNELYKKP 78
H.influenzae 86-028NP |YP_247808.1|     LLNSE-----------------LRQKYLNLLWQ-QVSMTQDMFNELYKKP 82
H.ducreyi 35000HP |NP_873395.1|         LLKTE-----------------LRQKYLNILWQ-QVSMTQDMFNSLYQRP 74
H.somnus 129PT |YP_718205.1|            LLNTE-----------------LRQHHLGLLWQ-QVSMTREMFEHLYQKP 75
M.aquaeolei VT8 |ZP_00817690.1|         LLKQP-----------------KRTELISRVKR-LFSVTEQVWNKHYLYA 83
A.a.citrulli AAC00-1 |ZP_01407598.1|    LLTTV-----------------QASRAIQEIWR-KSNQSRETWERDLLPA 124
Azoarcus EbN1 |YP_157225.1|             LIQVC-----------------NLAGALQQIHR-ESKLSQAVWERDFAPA 101
E.coli pAPEC-O1-R |ABF67837.1|          LYREKL----------------HSISMMLAISDSDIRDDAYTFTNLVLKP 116
S.marcescens R478 |NP_941280.1|         LYREKL----------------HSISMMLAISDSDIRDDAYTFTNLVLKP 116
S.typhi R27 |NP_058333.1|              LYRDKL----------------HSISMMLAISDGDIREDAYTFTNLVLKP 114
S.e.e.typhi CT18 pHCM1 |NP_569454.1|   LYRDKL----------------HSISMMLAISDGDIREDAYTFTNLVLKP 114
N.gonorrhoeae MS11 |AAW83058.1|         LIQVLD----------------LSPQISGIKMN--LGLSDENWSKDALPF 89
P.resinovorans pCAR1 |NP_758664.1|     LRYPPYQEGYPGLVSGQWFMRNYQHELFDRIIH-SVGMPASDLKLYVEPI 149
P.vulgaris UR-75 pRts1 |NP_640161.1|   FPAQVPG----------FALLSLQEEIISKIKR-ELMIRDAEYDEYIQPM 86
Consensus                              ..................................................
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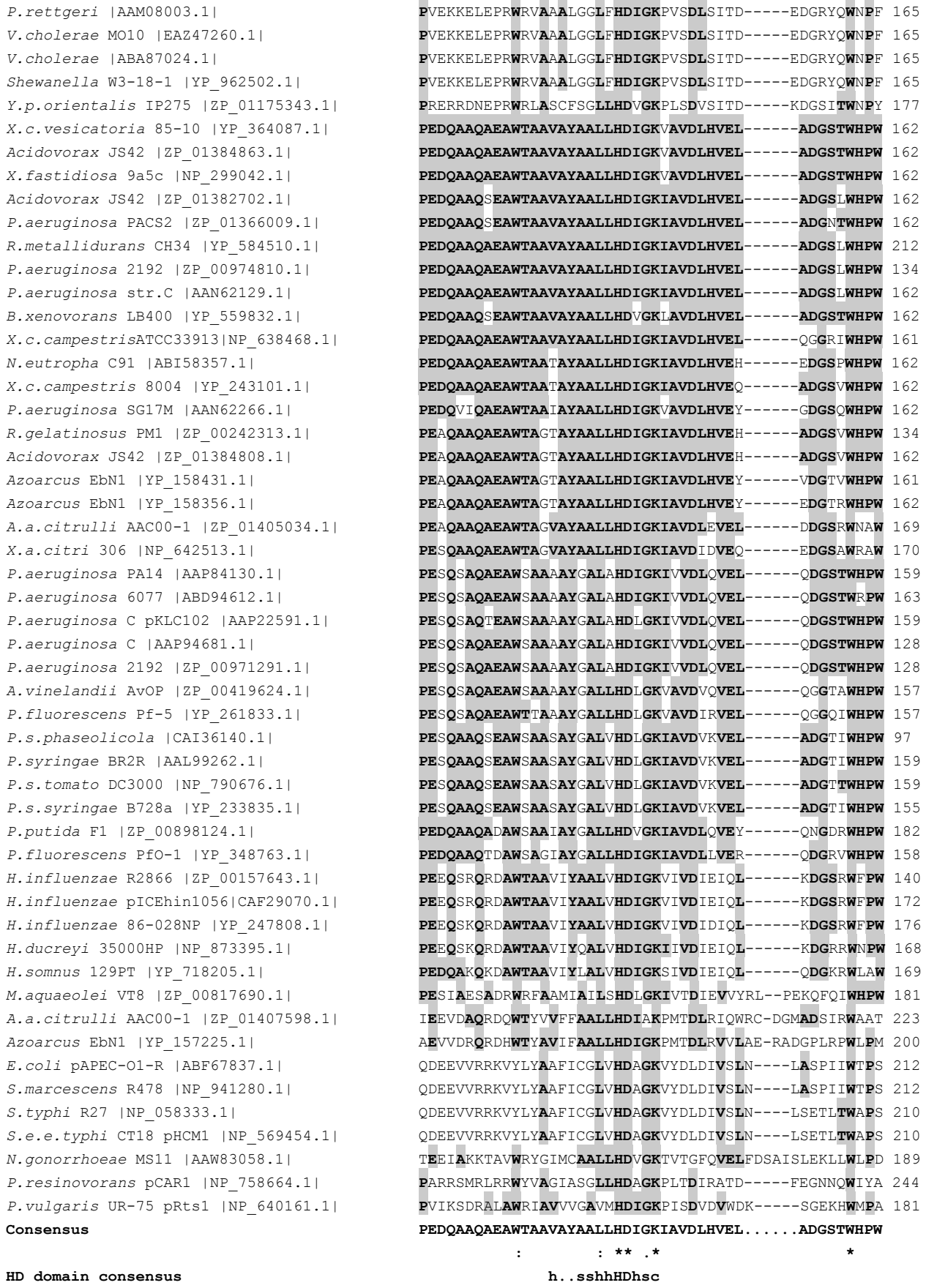
P.rettgeri |AAM08003.1|                    IDHLAAYVHLLPASEHHHHSGAGGLLRHSLEVAFWAAQAAEGIIFVASGT 120
V.cholerae MO10 |EAZ47260.1|              IDHLAAYVHLLPASEHHHHSGAGGLLRHSLEVAFWAAQAAEGIIFVASGT 120
V.cholerae |ABA87024.1|                   IDHLAAYVHLLPASEHHHHSGAGGLLRHSLEVAFWAAQAAEGIIFVASGT 120
Shewanella W3-18-1 |YP_962502.1|          IDHLAAYVHLLPASEHHHHSGAGGLLRHSLEVAFWAAQAAEGIIFVASGT 120
Y.p.orientalis IP275 |ZP_01175343.1|      IQRYAAFVHLLPASESHHHRGAGGLFRHGLEVAFWAAQASESVIFSIEGT 132
X.c.vesicatoria 85-10 |YP_364087.1|       LERYAELVQGFPASEAHHHAYLGGMLDHGLEIVAYGLKLRQSHLLPVGAS 118
Acidovorax JS42 |ZP_01384863.1|           LERYAELAQGFPASEAHHHAYLGGMLDHGLEIVAYGLKLRQSHLLPVGAS 118
X.fastidiosa 9a5c |NP_299042.1|           LERYAELVQVFPASEAHHHAYPGGMLDHGLEIVAYSLKLRQSHLLPIGAT 118
Acidovorax JS42 |ZP_01382702.1|           LERYAELVQAFPASEAHHHAYPGGMLDHGLEIVAYSLKLRQSHLLPIGAS 118
P.aeruginosa PACS2 |ZP_01366009.1|        LERYAELVQQFPASESHHHAYPGGMLDHGLEIVAYSLKLRQSHLLPIGAS 118
R.metallidurans CH34 |YP_584510.1|        LERYAELVQAFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPIGAS 168
P.aeruginosa 2192 |ZP_00974810.1|         LERYAELVQAFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPIGAS 90
P.aeruginosa str.C |AAN62129.1|           LERYAELVQAFPASESHHAYPGGMLDHGLEIVAYALKLRQSHHLLPIGAS 118
B.xenovorans LB400 |YP_559832.1|          LERYAELVQRFPASEAHHHAYPGGMLDHGLEIVAYALKLRQSHLLPAGST 118
X.c.campestrisATCC33913|NP_638468.1|     LERYADLVQQFPASESHHHAYLGGMLDHGLEIVAFALKLRQSHLLPAGAS 117
N.eutropha C91 |ABI58357.1|              LERYAELVQLFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPAGTT 118
X.c.campestris 8004 |YP_243101.1|        LERYAALVQQFSASESHHHAYHGGMLDHGLEIVAYALKLRQSYLLPAGAT 118
P.aeruginosa SG17M |AAN62266.1|          LERYASLVQQFPASESHHHAYSGGMLDHGLEIVAYALKLRQSYLLPTGTT 118
R.gelatinosus PM1 |ZP_00242313.1|        LERYAELVQQFPASENHHHAYPGGMLDHGLEIVAYALKLRQSYLLPAGVT 90
Acidovorax JS42 |ZP_01384808.1|          LERYAELVQQFPASENHHHAYPGGMLDHGLEIVAYALKLRQSYLLPAGVT 118
Azoarcus EbN1 |YP_158431.1|             LERYVELVQQFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPAGAT 117
Azoarcus EbN1 |YP_158356.1|             LERYAELVQQFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPAGAS 118
A.a.citrulli AAC00-1 |ZP_01405034.1|     IRRYAEFVQSFPASESHHHAYPGGMLDHGLEIVAYALKLRQSHLLPAGAT 125
X.a.citri 306 |NP_642513.1|              IQRYAEMVQLFPASESHHHAHPGGMLDHGLEIVAYALKLRQSYLLPAGAT 126
P.aeruginosa PA14 |AAP84130.1|           LANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAA 115
P.aeruginosa 6077 |ABD94612.1|           LANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAA 119
P.aeruginosa C pKLC102 |AAP22591.1|     LANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAA 115
P.aeruginosa C |AAP94681.1|             LANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAA 84
P.aeruginosa 2192 |ZP_00971291.1|        LANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAA 84
A.vinelandii AvOP |ZP_00419624.1|        LERFAELVQLLPASENHHHAHLGGLLDHGLEIVAYALKIRQTYLLPIGAP 113
P.fluorescens Pf-5 |YP_261833.1|         LERYAELVQLMPASENHHHAHLGGLLDHGLEIVAYALKIRQTYLLPIGAP 113
P.s.phaseolicola |CAI36140.1|           FKSYAALVQHLPASENHHHAYHGGMLDHGLEIVAYALKIRQMYLLPIGAP 53
P.syringae BR2R |AAL99262.1|            FKSYAALVQHLPASENHHHAYHGGMLDHGLEIVAYALKIRQMYLLPIGAP 115
P.s.tomato DC3000 |NP_790676.1|         FKSYAALVQHLPASENHHHAYHGGMLDHGLEIVAYALKIRQMYLLPIGAP 115
P.s.syringae B728a |YP_233835.1|        FKSYAALVQHLPASENHHHAYHGGMLDHGLEIVAYALKIRQMYLLPIGAP 111
P.putida F1 |ZP_00898124.1|             IRRYATYVQQLPASESHHHAYPGGMLDHGLELVACSLKLRQSYLLPGGAA 138
P.fluorescens PfO-1 |YP_348763.1|       IHRYAEQVQQLPASETHHHAYLGGMLDHGLELVACSLKLRQSYLLPTGAA 114
H.influenzae R2866 |ZP_00157643.1|      IERYAEMVQLLPASEAHHHSHLGGMLDHGLEVLSFATKLRQSYVLPQNAA 96
H.influenzae pICEhin1056|CAF29070.1|   IERYAEMVQLLPASEAHHHSHLGGMLDHGLEVLSFATKLRQSYVLPQNAA 128
H.influenzae 86-028NP |YP_247808.1|     IERYAEMVQLLPASESHHHSHLGGMLDHGLEVLSFAAKLRQSYVLPQNAA 132
H.ducreyi 35000HP |NP_873395.1|         IERYAEMVQLLPASEAHHHAPLGGMLDHGLEVLSFAAKLRQSYVLPQNAA 124
H.somnus 129PT |YP_718205.1|            IERYAEMVQLLPASESHHHSHLGGMLDHGLEVISFAAKLRQNYVLPLNAA 125
M.aquaeolei VT8 |ZP_00817690.1|         IEQFAELVQEVPASEIHHHSESGGLIDHTLEALYAGVRISQGYILPPNAE 133
A.a.citrulli AAC00-1 |ZP_01407598.1|    IHRYAEFVQLMPASEAHHHAHAGGLLSHTIEMLLAAMTWRNAHLLPGGSE 174
Azoarcus EbN1 |YP_157225.1|             IGQTLRYVQLLPASEAHHHAHVGGLAAHTVEVVHAAIAIRNGYLLPRGGA 151
E.coli pAPEC-O1-R |ABF67837.1|          LVEYVRWIHLLPASENHHHNGIGGLLSHSLEVAILSLKNAHHSELRPIGY 166
S.marcescens R478 |NP_941280.1|         LVEYVRWIHLLPASENHHHNGIGGLLSHSLEVAILSLKNAHHSELRPIGY 166
S.typhi R27 |NP_058333.1|              LIEYIRWIHLLPASENHHHNGIGGLLSHSLEVAMISLKNANHSELRPIGY 164
S.e.e.typhi CT18 pHCM1 |NP_569454.1|    LIEYIRWIHLLPASENHHHNGIGGLLSHSLEVAMISLKNANHSELRPIGY 164
N.gonorrhoeae MS11 |AAW83058.1|         LEKYIAFVQRLPASESHHHAGDGGLVRHTLDVAALALVASTSQSWPPNAK 139
P.resinovorans pCAR1 |NP_758664.1|      LVNFAELAHMLPASENHHHSGPGGLLRHSLEVASLTLDGCLTTAFDTNET 199
P.vulgaris UR-75 pRts1 |NP_640161.1|    LTNFANFVHLLPASEFHHHRAQGGLLRHTLEVVLYSIKIAKSFEFDANES 136
Consensus                                LERYAELVQLLPASE.HHHAYPGGMLDHGLEIVAYALKLRQSYLLPIGAT
                                         :        :..*** ***   ** : * ::
HD domain consensus                                            H.b.....s..h
```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V.cholerae MO10 |EAZ47260.1| PVEKKELEPRWRVAAALGGLFHDIGKPVSDLSITD-----EDGRYQWNPF 165
V.cholerae |ABA87024.1| PVEKKELEPRWRVAAALGGLFHDIGKPVSDLSITD-----EDGRYQWNPF 165
Shewanella W3-18-1 |YP_962502.1| PVEKKELEPRWRVAAALGGLFHDIGKPVSDLSITD-----EDGRYQWNPF 165
Y.p.orientalis IP275 |ZP_01175343.1| PRERRDNEPRWRLASCFSGLLHDVGKPLSDVSITD-----KDGSITWNPY 177
X.c.vesicatoria 85-10 |YP_364087.1| PEDQAAQAEAWTAAVAYAALLHDIGKVAVDLHVEL------ADGSTWHPW 162
Acidovorax JS42 |ZP_01384863.1| PEDQAAQAEAWTAAVAYAALLHDIGKVAVDLHVEL------ADGSTWHPW 162
X.fastidiosa 9a5c |NP_299042.1| PEDQAAQAEAWTAAVAYAALLHDIGKVAVDLHVEL------ADGSTWHPW 162
Acidovorax JS42 |ZP_01382702.1| PEDQAAQSEAWTAAVAYAALLHDIGKIAVDLHVEL------ADGSLWHPW 162
P.aeruginosa PACS2 |ZP_01366009.1| PEDQAAQSEAWTAAVAYAALLHDIGKIAVDLHVEL------ADGNTWHPW 162
R.metallidurans CH34 |YP_584510.1| PEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVEL------ADGSLWHPW 212
P.aeruginosa 2192 |ZP_00974810.1| PEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVEL------ADGSLWHPW 134
P.aeruginosa str.C |AAN62129.1| PEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVEL------ADGSLWHPW 162
B.xenovorans LB400 |YP_559832.1| PEDQAAQSEAWTAAVAYAALLHDVGKLAVDLHVEL------ADGSTWHPW 162
X.c.campestrisATCC33913|NP_638468.1| PEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVEL------QGGRIWHPW 161
N.eutropha C91 |ABI58357.1| PEDQAAQAEAWTAATAYAALLHDIGKIAVDLHVEH------EDGSPWHPW 162
X.c.campestris 8004 |YP_243101.1| PEDQAAQAEAWTAATAYAALLHDIGKIAVDLHVEQ------ADGSVWHPW 162
P.aeruginosa SG17M |AAN62266.1| PEDQVIQAEAWTAAIAYAALLHDIGKVAVDLHVEY------GDGSQWHPW 162
R.gelatinosus PM1 |ZP_00242313.1| PEAQAAQAEAWTAGTAYAALLHDIGKIAVDLHVEH------ADGSVWHPW 134
Acidovorax JS42 |ZP_01384808.1| PEAQAAQAEAWTAGTAYAALLHDIGKIAVDLHVEH------ADGSVWHPW 162
Azoarcus EbN1 |YP_158431.1| PEAQAAQAEAWTAGTAYAALLHDIGKIAVDLHVEY------VDGTVWHPW 161
Azoarcus EbN1 |YP_158356.1| PEAQAAQAEAWTAGTAYAALLHDIGKIAVDLHVEY------EDGTRWHPW 162
A.a.citrulli AAC00-1 |ZP_01405034.1| PEAQAAQAEAWTAGVAYAALLHDIGKIAVDLEVEL------DDGSRWNAW 169
X.a.citri 306 |NP_642513.1| PESQAAQAEAWTAGVAYAALLHDIGKIAVDIDVEQ------EDGSAWRAW 170
P.aeruginosa PA14 |AAP84130.1| PESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVEL------QDGSTWHPW 159
P.aeruginosa 6077 |ABD94612.1| PESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVEL------QDGSTWRPW 163
P.aeruginosa C pKLC102 |AAP22591.1| PESQSAQTEAWSAAAAYGALAHDLGKIVVDLQVEL------QDGSTWHPW 159
P.aeruginosa C |AAP94681.1| PESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVEL------QDGSTWHPW 128
P.aeruginosa 2192 |ZP_00971291.1| PESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVEL------QDGSTWHPW 128
A.vinelandii AvOP |ZP_00419624.1| PESQSAQAEAWSAAAAYGALLHDLGKVAVDVQVEL------QGGTAWHPW 157
P.fluorescens Pf-5 |YP_261833.1| PESQSAQAEAWTTAAAYGALLHDLGKVAVDIRVEL------QGGQIWHPW 157
P.s.phaseolicola |CAI36140.1| PESQAAQSEAWSAASAYGALVHDLGKIAVDVKVEL------ADGTIWHPW 97
P.syringae BR2R |AAL99262.1| PESQAAQSEAWSAASAYGALVHDLGKIAVDVKVEL------ADGTIWHPW 159
P.s.tomato DC3000 |NP_790676.1| PESQAAQSEAWSAASAYGALVHDLGKIAVDVKVEL------ADGTTWHPW 159
P.s.syringae B728a |YP_233835.1| PESQAAQSEAWSAASAYGALVHDLGKIAVDVKVEL------ADGTIWHPW 155
P.putida F1 |ZP_00898124.1| PEDQAAQADAWSAAIAYGALLHDVGKIAVDLQVEY------QNGDRWHPW 182
P.fluorescens PfO-1 |YP_348763.1| PEDQAAQTDAWSAGIAYGALLHDIGKIAVDLLVER------QDGRVWHPW 158
H.influenzae R2866 |ZP_00157643.1| PEEQSRQRDAWTAAVIYAALVHDIGKVIVDIEIQL------KDGSRWFPW 140
H.influenzae pICEhin1056|CAF29070.1| PEEQSRQRDAWTAAVIYAALVHDIGKVIVDIEIQL------KDGSRWFPW 172
H.influenzae 86-028NP |YP_247808.1| PEEQSKQRDAWTAAVIYAALVHDIGKVIVDIDIQL------KDGSRWFPW 176
H.ducreyi 35000HP |NP_873395.1| PEEQSKQRDAWTAAVIYQALVHDIGKIIVDIEIQL------KDGRRWNPW 168
H.somnus 129PT |YP_718205.1| PEDQAKQKDAWTAAVIYLALVHDIGKSIVDIEIQL------QDGKRWLAW 169
M.aquaeolei VT8 |ZP_00817690.1| PESIAESADRWRFAAMIAILSHDLGKIVTDIEVVYRL--PEKQFQIWHPW 181
A.a.citrulli AAC00-1 |ZP_01407598.1| IEEVDAQRDQWTYVVFFAALLHDIAKPMTDLRIQWRC-DGMADSIRWAAT 223
Azoarcus EbN1 |YP_157225.1| AEVVDRQRDHWTYAVIFAALLHDIGKPMTDLRVVLAE-RADGPLRPWLPM 200
E.coli pAPEC-O1-R |ABF67837.1| QDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLN----LASPIIWTPS 212
S.marcescens R478 |NP_941280.1| QDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLN----LASPIIWTPS 212
S.typhi R27 |NP_058333.1| QDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLN----LSETLTWAPS 210
S.e.e.typhi CT18 pHCM1 |NP_569454.1| QDEEVVRRKVYLYAAFICGLVHDAGKVYDLDIVSLN----LSETLTWAPS 210
N.gonorrhoeae MS11 |AAW83058.1| TEEIAKKTAVWRYGIMCAALLHDVGKTVTGFQVELFDSAISLEKLLWLPD 189
P.resinovorans pCAR1 |NP_758664.1| PARRSMRLRRWYVAGIASGLLHDAGKPLTDIRATD-----FEGNNQWIYA 244
P.vulgaris UR-75 pRts1 |NP_640161.1| PVIKSDRALAWRIAVVVGAVMHDIGKPISDVDVWDK-----SGEKHWMPA 181
Consensus PEDQAAQAEAWTAAVAYAALLHDIGKIAVDLHVEL......ADGSTWHPW
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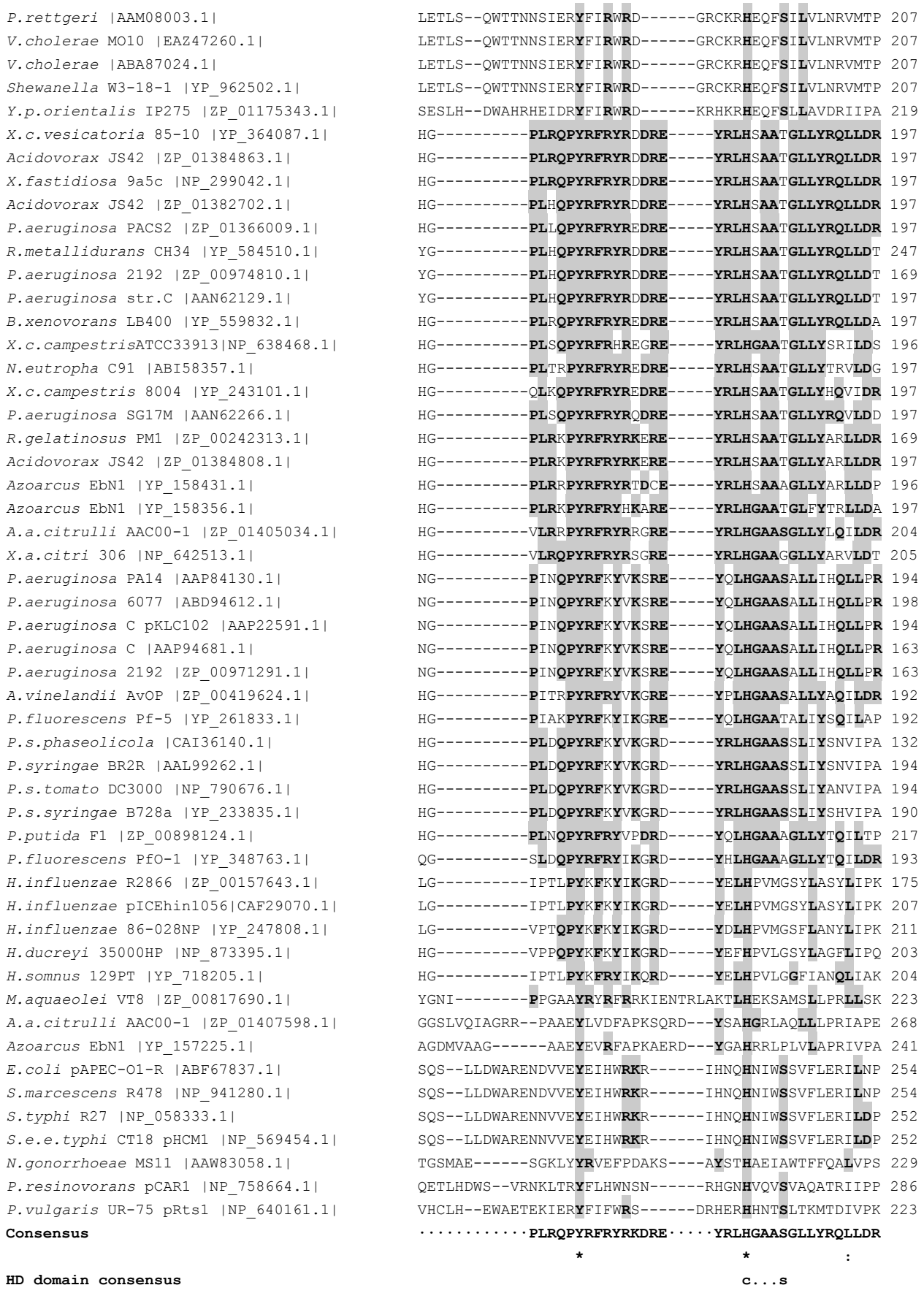
HD domain consensus h..sshhHDhsc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V.cholerae MO10 |EAZ47260.1| LETLS--QWTTNNSIERYFIRWRD------GRCKRHEQFSILVLNRVMTP 207
V.cholerae |ABA87024.1| LETLS--QWTTNNSIERYFIRWRD------GRCKRHEQFSILVLNRVMTP 207
Shewanella W3-18-1 |YP_962502.1| LETLS--QWTTNNSIERYFIRWRD------GRCKRHEQFSILVLNRVMTP 207
Y.p.orientalis IP275 |ZP_01175343.1| SESLH--DWAHRHEIDRYFIRWRD------KRHKRHEQFSLLAVDRIIPA 219
X.c.vesicatoria 85-10 |YP_364087.1| HG----------PLRQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDR 197
Acidovorax JS42 |ZP_01384863.1| HG----------PLRQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDR 197
X.fastidiosa 9a5c |NP_299042.1| HG----------PLRQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDR 197
Acidovorax JS42 |ZP_01382702.1| HG----------PLHQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDR 197
P.aeruginosa PACS2 |ZP_01366009.1| HG----------PLLQPYRFRYREDRE-----YRLHSAATGLLYRQLLDR 197
R.metallidurans CH34 |YP_584510.1| YG----------PLHQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDT 247
P.aeruginosa 2192 |ZP_00974810.1| YG----------PLHQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDT 169
P.aeruginosa str.C |AAN62129.1| YG----------PLHQPYRFRYRDDRE-----YRLHSAATGLLYRQLLDT 197
B.xenovorans LB400 |YP_559832.1| HG----------PLRQPYRFRYREDRE-----YRLHSAATGLLYRQLLDA 197
X.c.campestrisATCC33913|NP_638468.1| HG----------PLSQPYRFRHREGRE-----YRLHGAATGLLYSRILDS 196
N.eutropha C91 |ABI58357.1| HG----------PLTRPYRFRYREDRE-----YRLHSAATGLLYTRVLDG 197
X.c.campestris 8004 |YP_243101.1| HG----------QLKQPYRFRYREDRE-----YRLHSAATGLLYHQVIDR 197
P.aeruginosa SG17M |AAN62266.1| HG----------PLSQPYRFRYRQDRE-----YRLHSAATGLLYRQVLDD 197
R.gelatinosus PM1 |ZP_00242313.1| HG----------PLRKPYRFRYRKERE-----YRLHSAATGLLYARLLDR 169
Acidovorax JS42 |ZP_01384808.1| HG----------PLRKPYRFRYRKERE-----YRLHSAATGLLYARLLDR 197
Azoarcus EbN1 |YP_158431.1| HG----------PLRRPYRFRYRTDCE-----YRLHSAAAGLLYARLLDP 196
Azoarcus EbN1 |YP_158356.1| HG----------PLRKPYRFRYHKARE-----YRLHGAATGLFYTRLLDA 197
A.a.citrulli AAC00-1 |ZP_01405034.1| HG----------VLRRPYRFRYRRGRE-----YRLHGAASGLLYLQILDR 204
X.a.citri 306 |NP_642513.1| HG----------VLRQPYRFRYRSGRE-----YRLHGAAGGLLYARVLDT 205
P.aeruginosa PA14 |AAP84130.1| NG----------PINQPYRFKYVKSRE-----YQLHGAASALLIHQLLPR 194
P.aeruginosa 6077 |ABD94612.1| NG----------PINQPYRFKYVKSRE-----YQLHGAASALLIHQLLPR 198
P.aeruginosa C pKLC102 |AAP22591.1| NG----------PINQPYRFKYVKSRE-----YQLHGAASALLIHQLLPR 194
P.aeruginosa C |AAP94681.1| NG----------PINQPYRFKYVKSRE-----YQLHGAASALLIHQLLPR 163
P.aeruginosa 2192 |ZP_00971291.1| NG----------PINQPYRFKYVKSRE-----YQLHGAASALLIHQLLPR 163
A.vinelandii AvOP |ZP_00419624.1| HG----------PITRPYRFRYVKGRE-----YPLHGAASALLYAQILDR 192
P.fluorescens Pf-5 |YP_261833.1| HG----------PIAKPYRFKYIKGRE-----YQLHGAATALIYSQILAP 192
P.s.phaseolicola |CAI36140.1| HG----------PLDQPYRFKYVKGRD-----YRLHGAASSLIYSNVIPA 132
P.syringae BR2R |AAL99262.1| HG----------PLDQPYRFKYVKGRD-----YRLHGAASSLIYSNVIPA 194
P.s.tomato DC3000 |NP_790676.1| HG----------PLDQPYRFKYVKGRD-----YRLHGAASSLIYANVIPA 194
P.s.syringae B728a |YP_233835.1| HG----------PLDQPYRFKYVKGRD-----YRLHGAASSLIYSHVIPA 190
P.putida F1 |ZP_00898124.1| HG----------PLNQPYRFRYVPDRD-----YQLHGAAAGLLYTQILTP 217
P.fluorescens PfO-1 |YP_348763.1| QG----------SLDQPYRFRYIKGRD-----YHLHGAAAGLLYTQILDR 193
H.influenzae R2866 |ZP_00157643.1| LG----------IPTLPYKFKYIKGRD-----YELHPVMGSYLASYLIPK 175
H.influenzae pICEhin1056|CAF29070.1| LG----------IPTLPYKFKYIKGRD-----YELHPVMGSYLASYLIPK 207
H.influenzae 86-028NP |YP_247808.1| LG----------VPTQPYKFKYIKGRD-----YDLHPVMGSFLANYLIPK 211
H.ducreyi 35000HP |NP_873395.1| HG----------VPPQPYKFKYIKGRD-----YEFHPVLGSYLAGFLIPQ 203
H.somnus 129PT |YP_718205.1| HG----------IPTLPYKFRYIKQRD-----YELHPVLGGFIANQLIAK 204
M.aquaeolei VT8 |ZP_00817690.1| YGNI--------PPGAAYRYRFRRKIENTRLAKTLHEKSAMSLLPRLLSK 223
A.a.citrulli AAC00-1 |ZP_01407598.1| GGSLVQIAGRR--PAAEYLVDFAPKSQRD---YSAHGRLAQLLLPRIAPE 268
Azoarcus EbN1 |YP_157225.1| AGDMVAAG------AAEYEVRFAPKAERD---YGAHRRLPLVLAPRIVPA 241
E.coli pAPEC-O1-R |ABF67837.1| SQS--LLDWARENDVVEYEIHWRKR------IHNQHNIWSSVFLERILNP 254
S.marcescens R478 |NP_941280.1| SQS--LLDWARENDVVEYEIHWRKR------IHNQHNIWSSVFLERILNP 254
S.typhi R27 |NP_058333.1| SQS--LLDWARENNVVEYEIHWRKR------IHNQHNIWSSVFLERILDP 252
S.e.e.typhi CT18 pHCM1 |NP_569454.1| SQS--LLDWARENNVVEYEIHWRKR------IHNQHNIWSSVFLERILDP 252
N.gonorrhoeae MS11 |AAW83058.1| TGSMAE------SGKLYYRVEFPDAKS----AYSTHAEIAWTFFQALVPS 229
P.resinovorans pCAR1 |NP_758664.1| QETLHDWS--VRNKLTRYFLHWNSN------RHGNHVQVSVAQATRIIPP 286
P.vulgaris UR-75 pRts1 |NP_640161.1| VHCLH--EWAETEKIERYFIFWRS------DRHERHHNTSLTKMTDIVPK 223
Consensus ·····PLRQPYRFRYRKDRE·····YRLHGAASGLLYRQLLDR
* * :
HD domain consensus c...s

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P.rettgeri |AAM08003.1|                        ELLAWLTQPG-PEILQAMLEA----------IGNTDLEHVLS----KLVI 242
V.cholerae MO10 |EAZ47260.1|                  ELLAWLTQPG-PEILQAMLEA----------IGNTDPEHVLS----KLVI 242
V.cholerae |ABA87024.1|                       ELLAWLTQPG-PEILQAMLEA----------IGNTDPEHVLS----KLVI 242
Shewanella W3-18-1 |YP_962502.1|              ELLAWLTQPG-PEILQAMLEA----------IGNTDPEHVLS----KLVI 242
Y.p.orientalis IP275 |ZP_01175343.1|          ETREFLSKSG-PSIMEAMLEA----------ISGTSVNQPVT----KLML 254
X.c.vesicatoria 85-10 |YP_364087.1|           DLLDWLSGY--PSLWAPLLYV----------LAGQYEHAGVLG----ELVV 232
Acidovorax JS42 |ZP_01384863.1|               DLLDWLSGY--PSLWAPLLYV----------LAGQYEHAGVLG----ELVV 232
X.fastidiosa 9a5c |NP_299042.1|               DLLDWLSGY--PSLWAPLLYV----------LAGQYEHAGVLG----ELVV 232
Acidovorax JS42 |ZP_01382702.1|               DALDWLSGY--PDLWGPLLYV----------LAGQYEHAGVLG----ELVV 232
P.aeruginosa PACS2 |ZP_01366009.1|            HVLDWLSGY--PALWAPLLYV----------LAGQYEHAGVLG----ELVV 232
R.metallidurans CH34 |YP_584510.1|            QLLDWLSDY--RDLWGPLLYV----------LAGQYEHAGVLG----ELVV 282
P.aeruginosa 2192 |ZP_00974810.1|             QLLDWLSDY--RDLWGPLLYV----------LAGQYEHAGVLG----ELVV 204
P.aeruginosa str.C |AAN62129.1|               QLLDWLSDY--RDLWGPLLYV----------LAGQYEHAGVLG----ELVV 232
B.xenovorans LB400 |YP_559832.1|             QLLDWLSGY--PALWGPLLYV----------LAGQYEHAGVLG----ELVV 232
X.c.campestrisATCC33913|NP_638468.1|         AALDWLSGY--PALWSQLLYV----------LSGQYEHADMLG----ELVV 231
N.eutropha C91 |ABI58357.1|                   DILDWLNGF--PSLWSALLYV----------LAGQYEHAGVLG----ELVI 232
X.c.campestris 8004 |YP_243101.1|             FILDWLSGF--PSLWAALLYI----------MAGQYEHAGVLG----ELVI 232
P.aeruginosa SG17M |AAN62266.1|               RILDWLSRY--PPLWSALLYV----------LAGQYEHAGTLG----ELVI 232
R.gelatinosus PM1 |ZP_00242313.1|             DIFDWLSGY--PDLWAALLYV----------LAGQYEHAGTLG----ELVV 204
Acidovorax JS42 |ZP_01384808.1|               DIFDWLSGY--PDLWAALLYV----------LAGQYEHAGTLG----ELVV 232
Azoarcus EbN1 |YP_158431.1|                   GIFDWLSGY--PDVWAALLYV----------LAGQYEHAGTLG----ELVV 231
Azoarcus EbN1 |YP_158356.1|                   GIFDWLSGY--PDLWSALLYV----------LAGQYEHAGTLG----ELVA 232
A.a.citrulli AAC00-1 |ZP_01405034.1|          AILDWLSGY--PDLWRPLLYV----------LAGQHEHAGVLG----ELVV 239
X.a.citri 306 |NP_642513.1|                   GILDWLSGF--PDLWSPLLFV----------LAGQNEHAGVLG----ELVV 240
P.aeruginosa PA14 |AAP84130.1|                TALDWLSRF--PELWAQLIYL----------FAGQYEHAGILG----EIIV 229
P.aeruginosa 6077 |ABD94612.1|                TALDWLSRF--PELWAQLIYL----------FAGQYEHAGILG----EIIV 233
P.aeruginosa C pKLC102 |AAP22591.1|           TALDWLSRF--PELWAQLIYL----------FAGQYEHAGILG----EIIV 229
P.aeruginosa C |AAP94681.1|                   TALDWLSRF--PELWAQLIYL----------FAGQYEHAGILG----EIIV 198
P.aeruginosa 2192 |ZP_00971291.1|             TALDWLSRF--PELWAQLIYL----------FAGQYEHAGILG----EIIV 198
A.vinelandii AvOP |ZP_00419624.1|             NILDWLSGF--PEPWRLLIYA----------LAGQYEHAGILG----EIVV 227
P.fluorescens Pf-5 |YP_261833.1|              EILDWLCGF--PELWTELIYL----------VAGQFENAGILG----EIVI 227
P.s.phaseolicola |CAI36140.1|                 KALDWLSGF--PELWSQLVFA----------FAGQYEHADILG----EIVS 167
P.syringae BR2R |AAL99262.1|                  KALDWLSGF--PELWSQLVFT----------FAGQYEHADILG----EIVS 229
P.s.tomato DC3000 |NP_790676.1|               KALDWLSGF--PELWTQLVFA----------FAGQYEHADILG----EIVS 229
P.s.syringae B728a |YP_233835.1|              KALDWLSGF--PELWSQLVFAFAFA-----FAGQYEHADILG----EIVS 229
P.putida F1 |ZP_00898124.1|                   TLLDWLSSY--PELWRQLLSL----------LADHYEQAGTLG----ELVL 252
P.fluorescens PfO-1 |YP_348763.1|             PILDWLSGF--PPLWASLLYV----------LAGQYERAGVLG----ELVM 228
H.influenzae R2866 |ZP_00157643.1|            EAFEWLAGY--PEAFASLMYA----------MANHKDKSGLLS----EIVQ 210
H.influenzae pICEhin1056|CAF29070.1|         EAFEWLAGY--PEAFASLMYA----------MANHKDKSGLLS----EIVQ 242
H.influenzae 86-028NP |YP_247808.1|           EAFAWLAEY--PEAFSALMYA----------MADHKDKAGLLS----EIVQ 246
H.ducreyi 35000HP |NP_873395.1|               EAFDWLTQY--PEVFS---------------------------------- 217
H.somnus 129PT |YP_718205.1|                  ETFDWLATY--PEVFSALMYA----------MAGHYDKANVLA----EIVQ 239
M.aquaeolei VT8 |ZP_00817690.1|               EAATWLFKD--LELISQLFST----------ISHSTFGGQVIA----EIVR 258
A.a.citrulli AAC00-1 |ZP_01407598.1|          SALQFLAYT--PAALDALEKY----------LSGQ-DKDSLVA----QIVK 302
Azoarcus EbN1 |YP_157225.1|                   TALAFLARE--PSVMLELQAV----------WSGD-DATSVLT----EIVR 275
E.coli pAPEC-O1-R |ABF67837.1|                VCLAFLDRVNKERVYSKMITA----------LNVYTDGNDFLS----KCVR 291
S.marcescens R478 |NP_941280.1|               VCLAFLDRVNKERVYSKMITA----------LNVYTDGNDFLS----KCVR 291
S.typhi R27 |NP_058333.1|                     VCMSFLDRVKKERVYAKMVTA----------LNVYNDGNDFLS----KCVR 289
S.e.e.typhi CT18 pHCM1 |NP_569454.1|          VCMSFLDRVKKERVYAKMVTA----------LNVYNDGNDFLS----KCVR 289
N.gonorrhoeae MS11 |AAW83058.1|               HVRQWLATTD-PNLMITLRNY----------LSGKKDGSPLE----QLIK 264
P.resinovorans pCAR1 |NP_758664.1|            AVQAWLIEGG-HDIYEALLDA-----------ISGSGSSPLT----ELVK 320
P.vulgaris UR-75 pRts1 |NP_640161.1|          SLLAFLMQEG-NDIYNELTEALAGSNSFRAVTSRNETGTVFKNKIHKIVA 272
Consensus                                      ··LDWL·····································ELVV
                                                  :*
HD domain consensus                               .h                                      ..h.
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P.rettgeri |AAM08003.1|                          EADQTSVQRDLKAQRISVDDNALG-VPVERYLLDAMRRLLASS-QWLVNQ 290
V.cholerae MO10 |EAZ47260.1|                    EADQTSVQRDLKAQRISVDDNALG-VPVERYLLDAMRRLLASS-QWLVNQ 290
V.cholerae |ABA87024.1|                          EADQTSVQRDLKAQRISVDDNALG-VPVERYLLDAMRRLLASS-QWLVNQ 290
Shewanella W3-18-1 |YP_962502.1|                 EADQTSVQRDLKAQRISVDDNALG-VPVERYLLDAMRRLLASS-QWLVNQ 290
Y.p.orientalis IP275 |ZP_01175343.1|             RADQESVSRDLRQSRLDVDEFSYG-VPVERYVFDAIRRLVKTG-KWKVNE 302
X.c.vesicatoria 85-10 |YP_364087.1|              QADRASVAQELGGDP-ARAMAAPK-HSLQRKLVNGLRYLLKE--ELKLNQ 278
Acidovorax JS42 |ZP_01384863.1|                  QADRASVAQELGGDP-ARAMAAPK-HSLQRKLVNGLRYLLKE--ELKLNQ 278
X.fastidiosa 9a5c |NP_299042.1|                  QADRASVAQELGGDP-ARAMAAPK-HSLQRKLVNGLRYLLKE--ELKLNQ 278
Acidovorax JS42 |ZP_01382702.1|                  QADRASVAQELGGDP-ARAMAAPK-HALQRKLLDGLRYLLKE--QLKLNQ 278
P.aeruginosa PACS2 |ZP_01366009.1|               QADRASVAQELGGDP-ARVMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 278
R.metallidurans CH34 |YP_584510.1|               QADRASVAQELGGDP-ARAMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 328
P.aeruginosa 2192 |ZP_00974810.1|                QADRASVAQELGGDP-ARAMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 250
P.aeruginosa str.C |AAN62129.1|                  QADRASVAQELGGDP-ARAMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 278
B.xenovorans LB400 |YP_559832.1|                 QADRASVAQELGGDP-ARAMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 278
X.c.campestrisATCC33913|NP_638468.1|            QADRASVAQELGGDP-AKVMAAPK-HALQRKLLEGLRYLLKE--QLKLNQ 277
N.eutropha C91 |ABI58357.1|                     QADRASVAQALGGDP-ARAMAAPK-HALQRKLLEGLRYLLKE--ELKLNQ 278
X.c.campestris 8004 |YP_243101.1|                KADRASVAQELGGDP-AKAMAAPK-HALQRKLLDGLRYLLKE--ELKLNQ 278
P.aeruginosa SG17M |AAN62266.1|                  QADRASVAQALGGDP-ARAMAAPK-HALQRKLLEGLRYLLKE--ELKLNQ 278
R.gelatinosus PM1 |ZP_00242313.1|                QADQASVAQELGGDP-SKALAAPK-HALQRKLLDGLRYLLKE--EFKLNQ 250
Acidovorax JS42 |ZP_01384808.1|                  QADQASVAQELGGDP-SKALAAPK-HALQRKLLDGLRYLLKE--EFKLNQ 278
Azoarcus EbN1 |YP_158431.1|                      QADRASVAQELGGDP-GKALAAPR-HALQRKLLDGLRFLLKE--EFKLNQ 277
Azoarcus EbN1 |YP_158356.1|                      QADQASVAQALGGDP-AKALAAPR-HALQRKLLDGLRYLLKE--EFKLNQ 278
A.a.citrulli AAC00-1 |ZP_01405034.1|             QADQASVAQAMGGDP-ARALAAPR-HALQRKLLDGLRFLLRE--QLQLNQ 285
X.a.citri_306_NP_642513.1                        QADQASVAQSLGGDP-AKALTAPR-HALQRKLLEGLRYLLRE--QLQINQ 286
P.aeruginosa PA14 |AAP84130.1|                   KADQASVAQELGGNP-DRALAAPK-QSLQRQLADGLRFLVKD--KFKLNQ 275
P.aeruginosa 6077 |ABD94612.1|                   KADQASVAQELGGNP-DRALAAPK-QSLQRQLADGLRFLVKD--KFKLNQ 279
P.aeruginosa C pKLC102 |AAP22591.1|              KADQASVAQELGGNP-DRALAAPK-QSLQRQLADGLRFLVKD--KFKLNQ 275
P.aeruginosa C |AAP94681.1|                     KADQASVAQELGGNP-DRALAAPK-QSLQRQLADGLRFLVKD--KFKLNQ 244
P.aeruginosa 2192 |ZP_00971291.1|                KADQASVAQELGGNP-DRALAAPK-QSLQRQLADGLRFLVKD--KFKLNQ 244
A.vinelandii AvOP |ZP_00419624.1|                KADQASVAQALGGNP-ERALAAPK-QSLQRQLAEGLRYLVRE--KFKLNQ 273
P.fluorescens Pf-5 |YP_261833.1|                 KADSASVAQELGGNP-DRAMAAPK-QSLQRQLVECLRYLVRE--KFKLNH 273
P.s.phaseolicola |CAI36140.1|                    QADQASVAQELGGNP-GRAMSAPK-QSIQRQLAEGLRVLVAD--KFKLNQ 213
P.syringae BR2R |AAL99262.1|                     QADQASVAQELGGNP-GRAMSAPK-QSIQRQLAEGLRMLVAD--KFKLNQ 275
P.s.tomato DC3000 |NP_790676.1|                  QADQASVAQELGGNP-GRAMSAPK-QSIQRQLAEGLRMLISE--KFKLNQ 275
P.s.syringae B728a |YP_233835.1|                 QADQASVAQELGGNP-GKAMSAPK-QSIQRQLAEGLRMLVAD--KFKLNQ 275
P.putida F1 |ZP_00898124.1|                      QADRVSTAQNIGANP-TKALQAPK-HSLQHHLLMGLRHLVKN--EFKLNQ 298
P.fluorescens PfO-1 |YP_348763.1|                QADRVSTAQNIGGNP-SKALQAPI-HSLQHHLISGLRHLVQH--ELKLNQ 274
H.influenzae R2866 |ZP_00157643.1|               KADQNSVTLALGGDV-SKLVQKPG-TSFTKQIVMALRYLLEH--KFKINT 256
H.influenzae pICEhin1056|CAF29070.1|             KADQNSVTLALGGDV-SKLVQKPG-TSFAKQIVMALRYLLEH--KFKINT 288
H.influenzae 86-028NP |YP_247808.1|              KADQNSVTLALGGDV-SKLTQKPI-TSFAKQLVMALRHLLQH--KFKINT 292
H.ducreyi 35000HP |NP_873395.1|                  --------------------------------------------------
H.somnus 129PT |YP_718205.1|                     KADQNSVALALGGDI-TKLVQKPV-ISFAKQLILALRYLISQ--KFKISS 285
M.aquaeolei VT8 |ZP_00817690.1|                  AADGASVSKNVGANTGKKADHTNT-IPLYEKLIVSLRKLVNDG-DLKRNK 306
A.a.citrulli AAC00-1 |ZP_01407598.1|             RADKLSTQRALLSGHKARFSTAKA-VPLIDLLMQAMAAMLRSGSTLPLNR 351
Azoarcus EbN1 |YP_157225.1|                      LADRRSAASNLQQGPRSQFSAATT-VPLIEQLMAAMRRLLRQG-GLPLNR 323
E.coli pAPEC-O1-R |ABF67837.1|                   TADFYSTGTDLNVLR-DPIMGLRS-NDAAARAISTIKHNFTS---ININN 336
S.marcescens R478 |NP_941280.1|                  TADFYSTGTDLNVLR-DPIMGLRS-NDAAARAISTIKHNFTS---ININN 336
S.typhi R27 |NP_058333.1|                        TSDYYSTGTDLNVLR-DPIMGLRS-NDAAARAIGTIKHNFTS---ININN 334
S.e.e.typhi CT18 pHCM1 |NP_569454.1|              TSDYYSTGTDLNVLR-DPIMGLRS-NDAAARAIGTIKHNFTS---ININN 334
N.gonorrhoeae MS11 |AAW83058.1|                  NADMTSVSRDLRSGSRQRFSTAKR-KPFIETIMETLKEMLSDR-GVHFSI 312
P.resinovorans pCAR1 |NP_758664.1|               WADSASTKRDLNRGSNNGGGNATG-VPVPRLVSDAMLRLLSDG-TWKINT 368
P.vulgaris UR-75 pRts1 |NP_640161.1|             HADSRSVKQDLQRYSGDAVRASQTGVPVIARIVDAMRLLIKKE-EWKPNQ 321
Consensus                                        QADQAS.....................................
                                                   *  *
HD domain consensus                              .hD.h.
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Fig. S1. CLUSTAL W alignment of the first three-hundred amino acids of proteins in the *Ng* TraI family. The different font colors represent proteins with similar predicted amphipathic α helices at the N-terminus proximal region: bold, green, blue, and magenta. Underlined (red) in *Ng* TraI is the unique N-terminal hydrophobic region, where the black background, white font highlights the N-terminal amphipathic α helix. *Azoarcus* sp. EbN1 (red font) contains an N-terminal transmembrane domain besides the N-terminus proximal amphipathic α helix. The predicted amphipathic α helices of proteins with two at the N-terminus proximal region are highlighted in yellow. It is not clear if *H. somnus* contains an amphipathic α helix since a charged reside (His) is present on the hydrophobic side of the predicted α helix (orange background, black font). Underlined in black is motif I and II of classical relaxases, present only in *E. coli* pAPEC-01-R, *S. marcescens* R478, *S. typhi* R27, and *S. typhi* CT18 pHCMI. Tyr^{93} and Tyr^{201} (in *N. gonorrhoeae*) are conserved. The His-rich motif, reported as motif III in R27 TraI, is a hallmark of this family of sequence h(Q/H)xhPASExHHHx_3GG(L/M)h, where h is a hydrophobic residue and x is any residue. The consensus sequence of the fifty-four proteins is shown. The consensus amino acid sequence for the HD domain is also shown: (b) big, (s) small, (h) hydrophobic, and (c) charged. The capital letters represent the invariant amino acids.